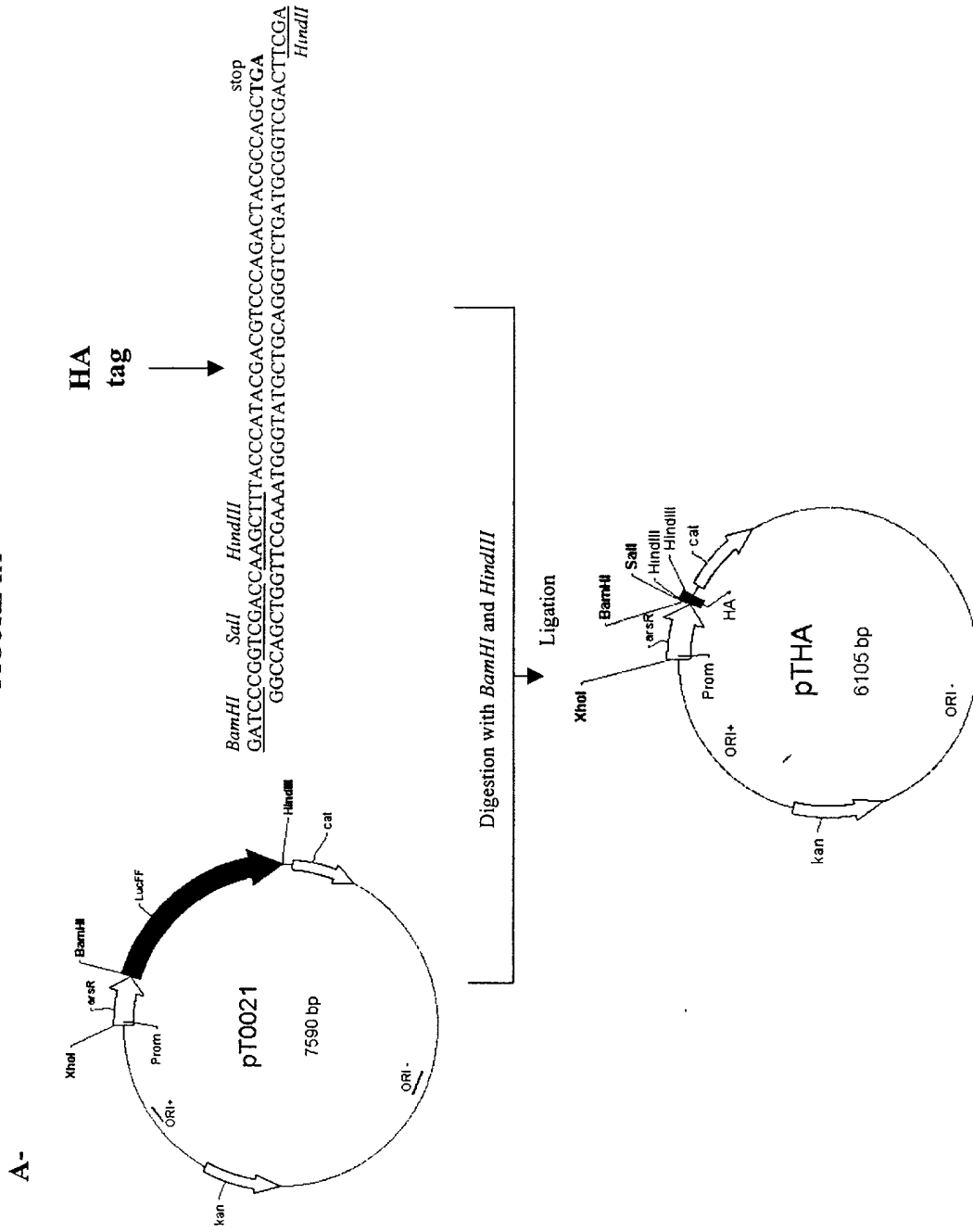


FIGURE 1A



B-

FIGURE 1B

PCR of pT0021 with XhoF and BamHNR

XhoF-5'-AATTCTCGAGTAAAATAACAT-3
XhoI

AAATCAGGTGACTGTTGAGAAAAGGAGGCGGATCCCG-BamHNR
Stop of
arsR RBS BamHI

Digestion with XhoI and BamHI

Ligation

PCR of pT0021 with LucFFB and LucFFH

LucFFB-5'-CGGGATCCATGAGGGGTTCCGAAGACG
BamHI Start Original BamHI
of LucFF was modified

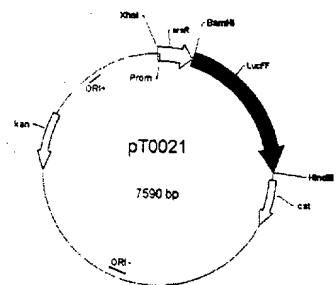
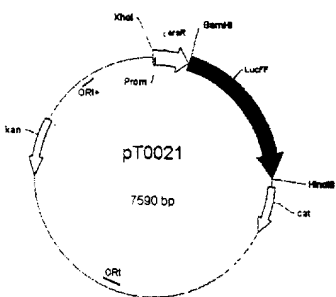
GAAAGTCCAAATTGTAAGCTTGGG-LucFFH
Stop of HindIII
LucFF

Digestion with BamHI and HindIII

Ligation

- Modified in the vicinity of BamHI
- Cloning site for ORFs: BamHI and HindIII
- No additional codons in the induced protein

Prom arsR LucFF
CTCGAG-----ATG-----TGAGAAAAGGAGGCGGATCCATG-----TAAGCTT
XhoI RBS BamHI HindIII



Modified between stop
of arsR to BamHI

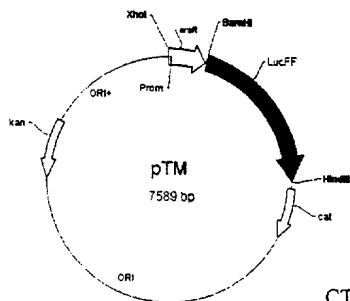
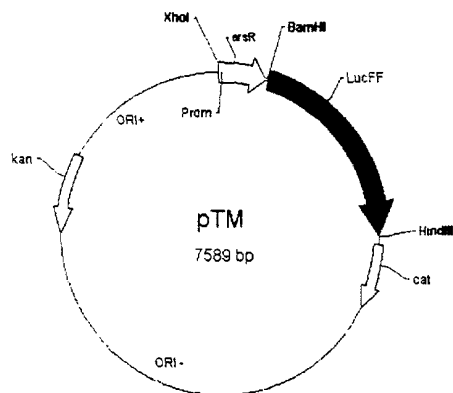


FIGURE 1C

C-



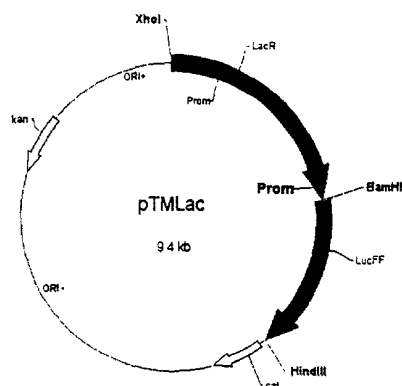
PCR of *Staphylococcus aureus* DNA
with lacF and LacR

LacF-5'-CCGCTCGAGCTCCAAATCCAAAACAG
XhoI

GTAAAAAGGAGTCTTATTGGATCCCG-LacR
BamHI

Digestion with *XhoI* and *BamHI*

Ligation



Prom LacR Prom LacA
 CTCGAG-----TTG-----CTA-----AGGAGTCTTATTGGATCCATG
XhoI *BamHI*

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FIGURE 2A

A-

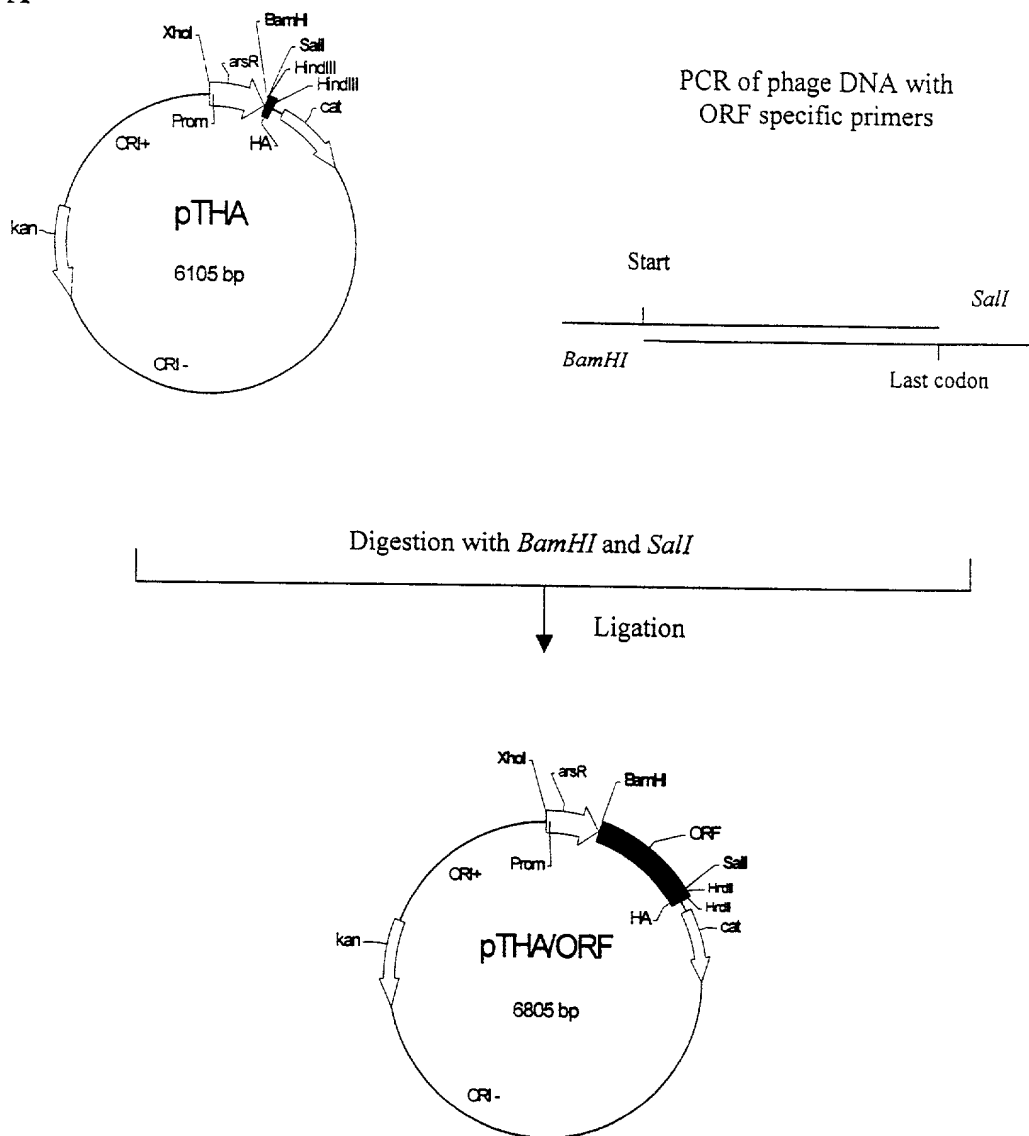
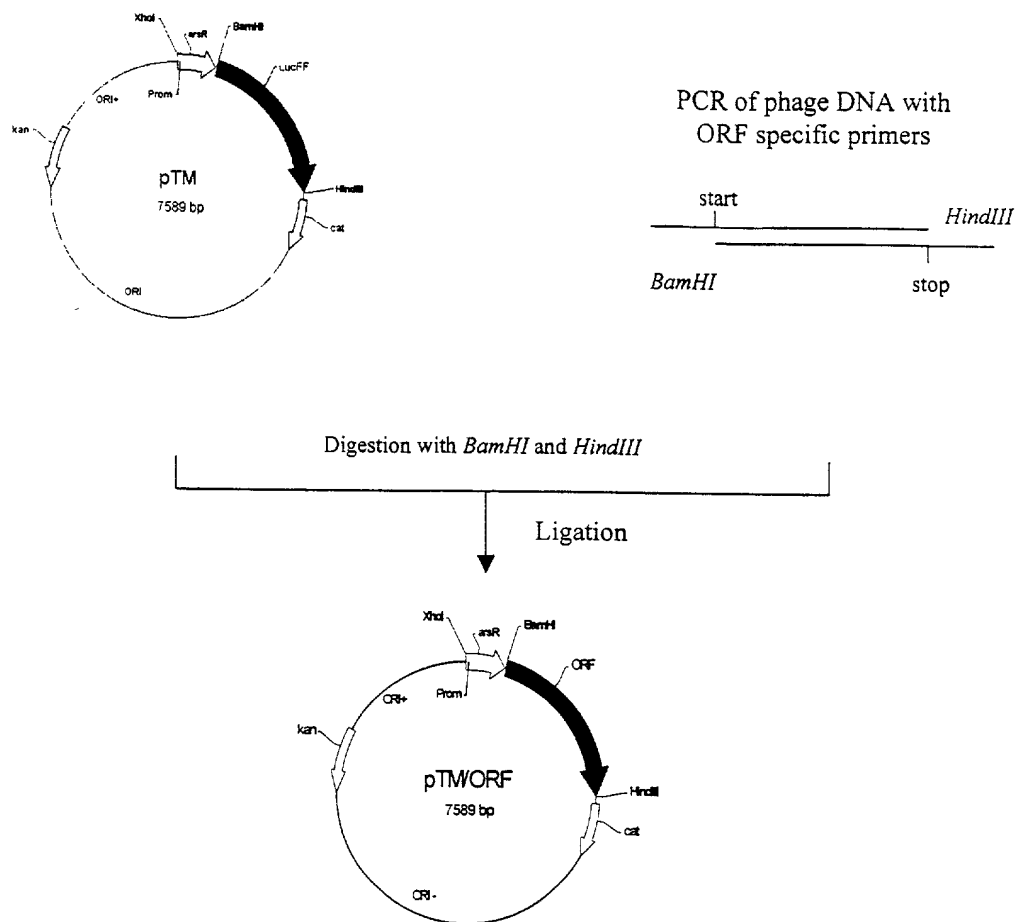


FIGURE 2B

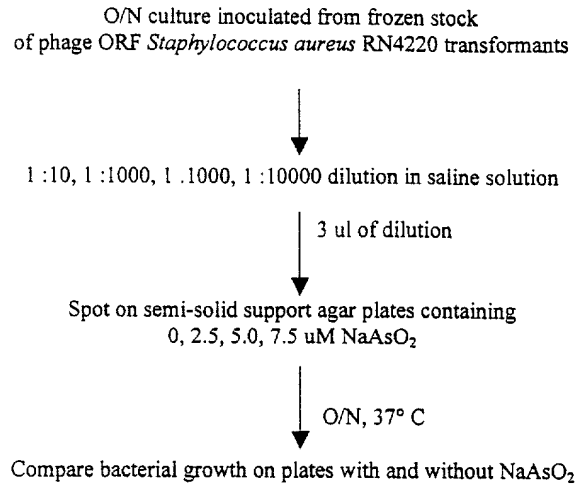
B-



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FIGURE 3

A) Functional assay on semi-solid support medium



B) Functional assay in liquid medium

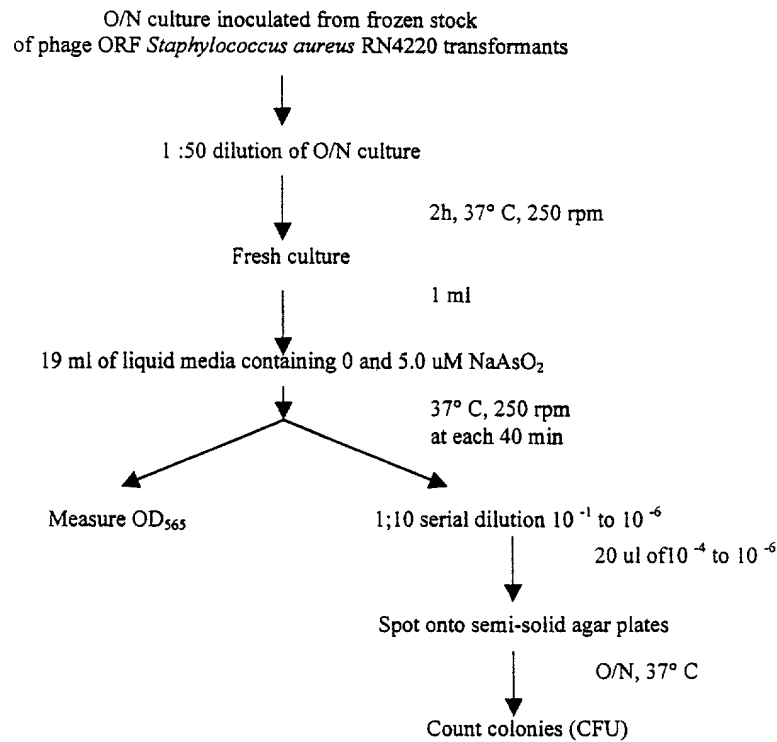


FIGURE 4A

A-

44AHJD ORFs tested for functional analysis

UID	POS
44AHJDORF001	12627..10342
44AHJDORF002	3789..5732
44AHJDORF003	6626..8389
44AHJDORF004	8764..10227
44AHJDORF005	13890..12643
44AHJDORF006	803..2029
44AHJDORF007	2044..3027
44AHJDORF008	3020..3775
44AHJDORF009	5744..6496
44AHJDORF010	14420..13938
44AHJDORF011	15593..15225
44AHJDORF012	8391..8813
44AHJDORF013	14996..14586
44AHJDORF019	9836..9630
44AHJDORF023	6494..6315
44AHJDORF025	15175..14999
44AHJDORF027	12916..13080
44AHJDORF028	9235..9071
44AHJDORF035	13957..13811
44AHJDORF036	10165..10019
44AHJDORF039	1743..1883
44AHJDORF040	9740..9877
44AHJDORF044	12917..12783
44AHJDORF046	4891..5019
44AHJDORF048	15340..15212
44AHJDORF049	5784..5909
44AHJDORF053	3348..3467
44AHJDORF113	199..600
44AHJDORF114	16172..15870
44AHJDORF121	16362..16165
44AHJDORF123	614..796

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B.

REF ID	Study, species adults transformants	Adult number	Date received 6-17-90 at 18:00 h
UAF-DORF2	Cone1		
	Cone2		
	Cone3		
UAF-DORF25	Cone1		
	Cone2		
	Cone3		
Contro. TOR=30	Cone1		

A-

FIGURE 5A

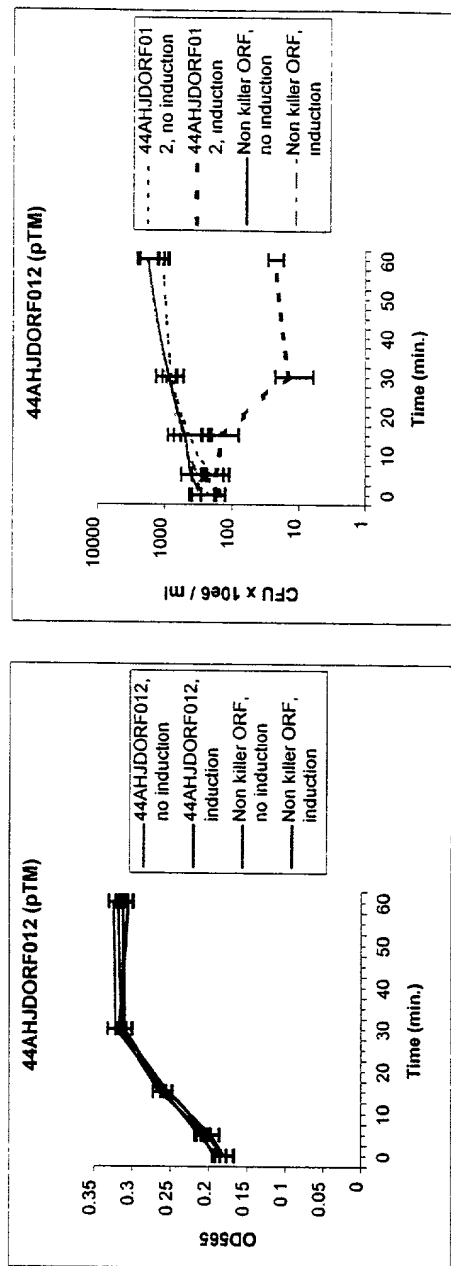


Fig
.5B

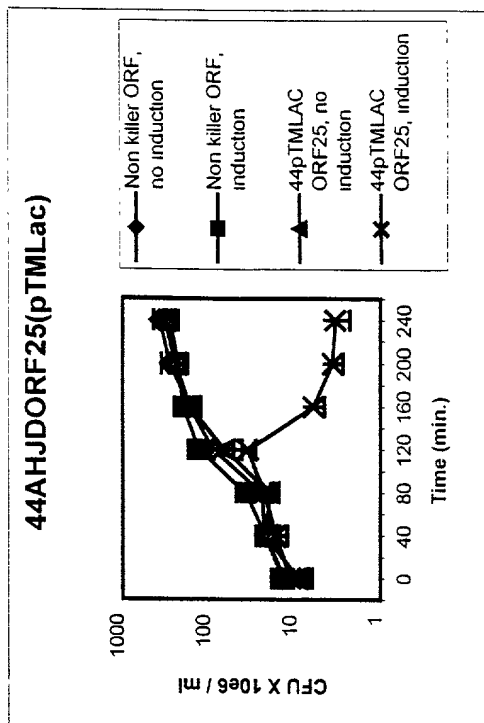
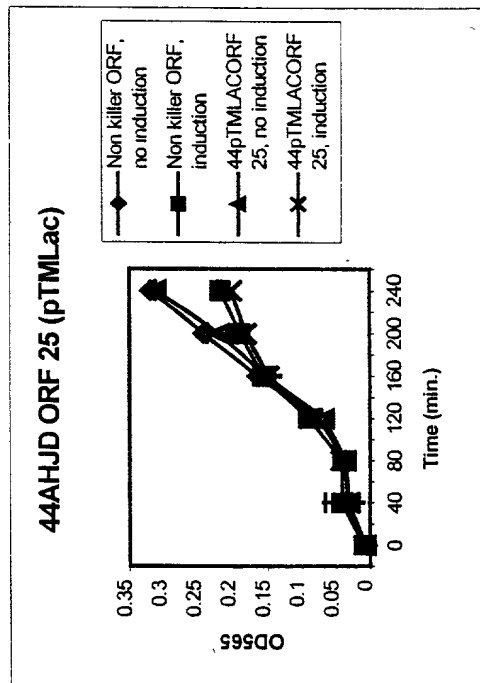
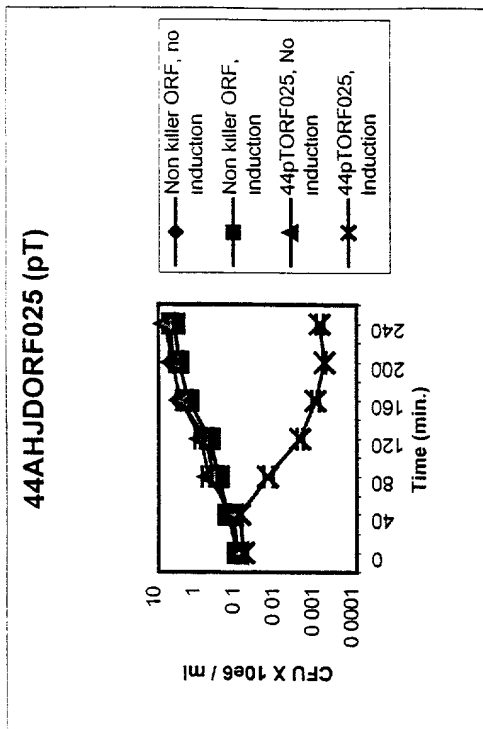
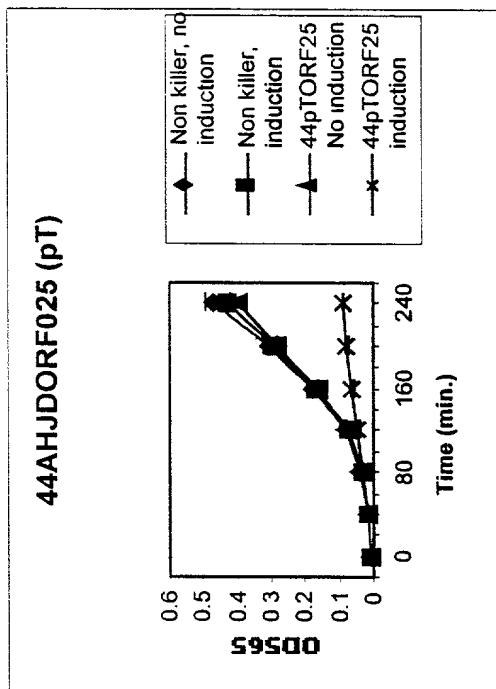
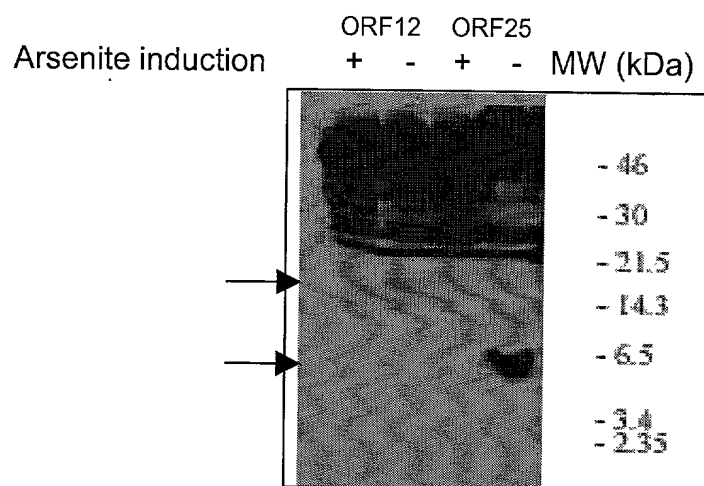


FIGURE 6



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FIGURE 7A

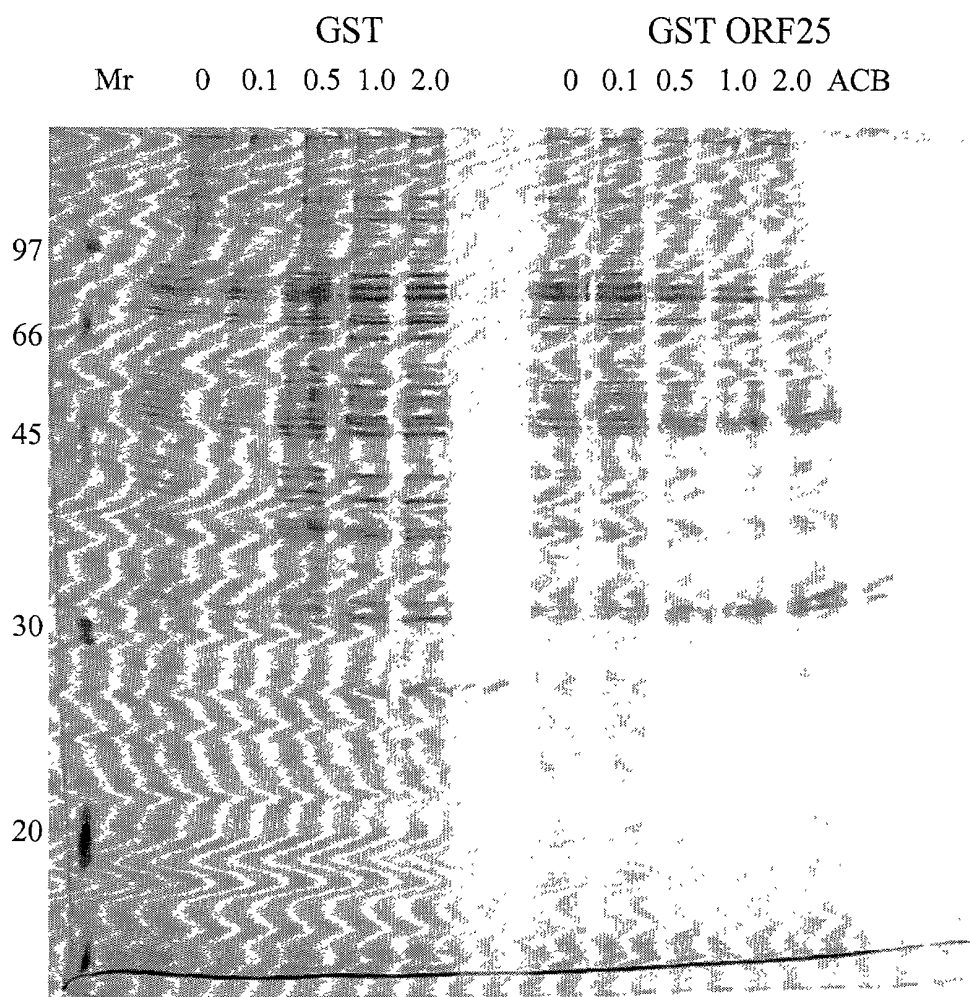
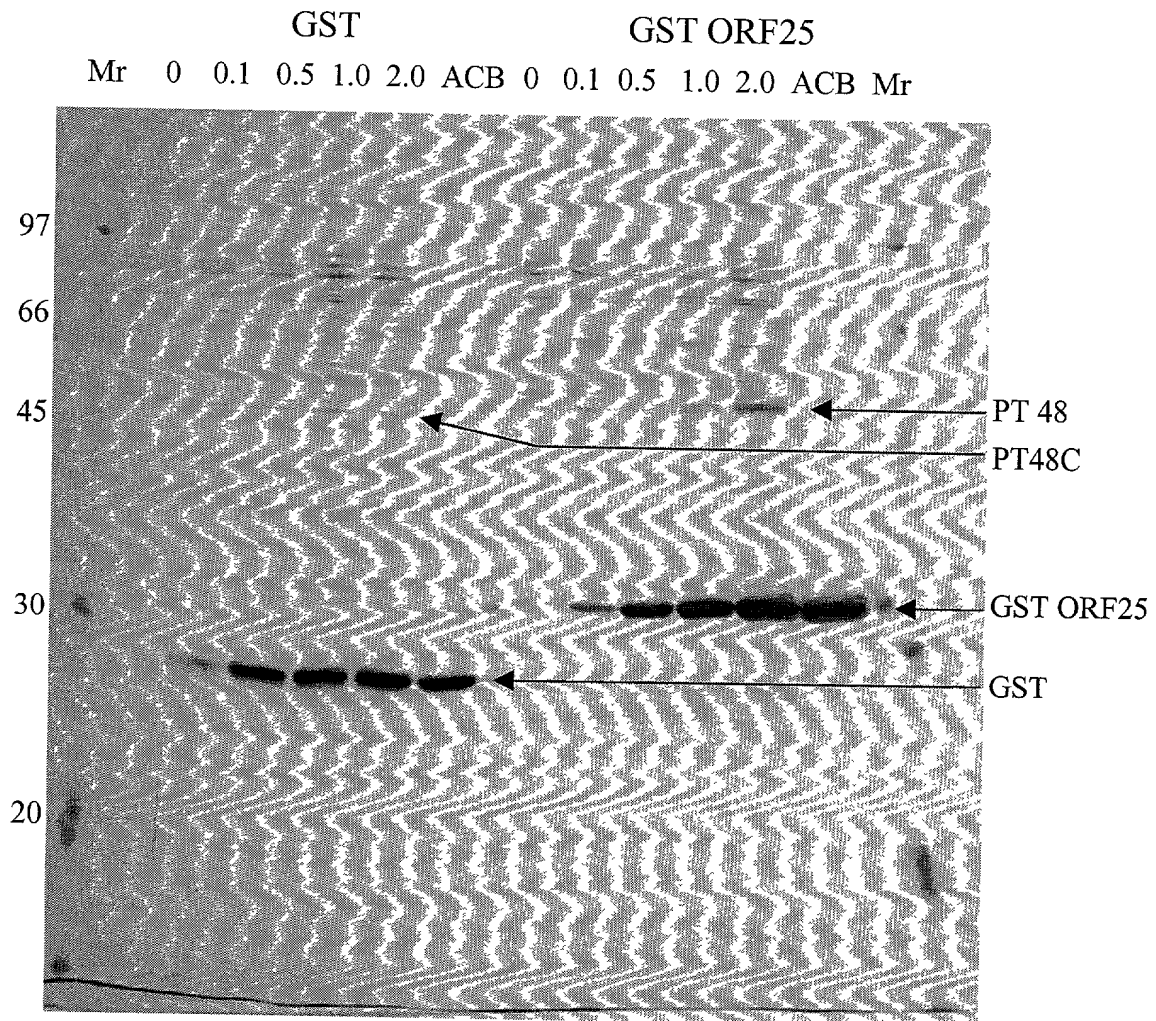


FIGURE 7B



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FIGURE 8

Tryptic peptide mass spectrum of 48 kDa interacting protein

(from Figure 1B)

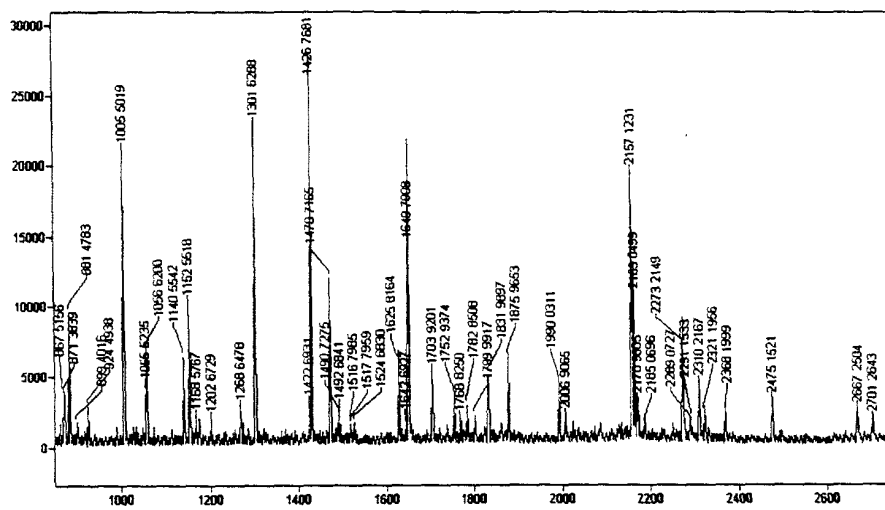
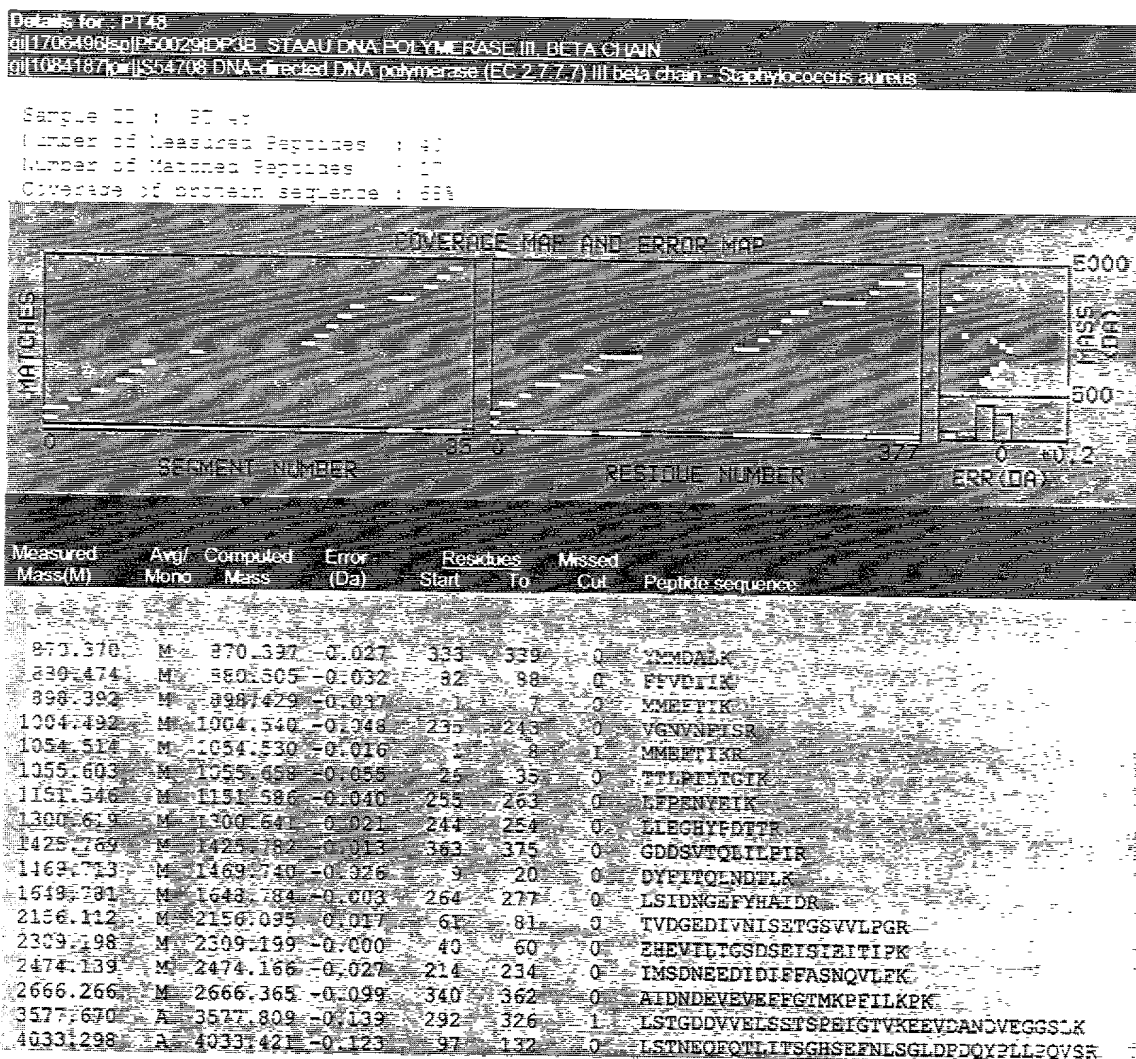


FIGURE 9

Identification of PT48 as DNA-directed DNA polymerase III beta.



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FIGURE 10

SEQ ID NO : 1 *Staphylococcus aureus* DnaN nucleotide sequence

ATGATGGAATTCATAAAGAGATTATTTTATTACACAATTAAATGACACATTAAAA
GCTATTTACCAAGAACAACATTACCTATATTAAGTGGTATCAAAATCGATGCGAAAGAA
CATGAAGTTATATTAAGTGGTTCAGACTCTGAAATTTCAATAGAAATCACTATTCCTAAA
ACTGTAGATGGCGAAGATATTGTCAATTTTCAGAAACAGGCTCAGTAGTACTTCCTGGA
CGATTCTTTGTTGATATTATAAAAAAATTACCTGGTAAAGATGTTAAATTATCTACAAAT
GAACAATTCAGACATTAATTACATCAGGTCATTCTGAATTTAATTAAAGTGGCTTAGAT
CCAGATCAATATCCTTTATTACCTCAAGTTTCTAGAGATGACGCAATTCAATTGTCGGTA
AAAGTGCTTAAAAACGTGATTGCACAAACAAATTTTGCAGTGTCCACCTCAGAAACACGC
CCAGTACTAAGTGGTGTGAAGTGGCTTATACAAGAAATGAATTAATATGCACAGCGACT
GACTCACACCGCTTGGCTGTAAGAAAGTTGCAGTTAGAAGATGTTTCTGAAAACAAAAAT
GTCATCATTCCAGGTAAGGCTTAGCTGAATTAATAAAATTATGTCTGACAATGAAGAA
GACATTGATATCTTCTTTGCTTCAAACCAAGTTTATTTAAAGTTGGAAATGTGAACCTT
ATTTCTCGATTATTAGAAGGACATTATCCTGATACAACACGTTTATTCCTGAAAACAT
GAAATTAATAAGTATAGACAATGGGGAGTTTATCATGCGATTGATCGTGCCTCTTTA
TTAGCGCGTGAAGGTGGTAATAACGTTATTAATAAGTACAGGTGATGACGTTGTTGAA
TTGTCTTCTACATCACCAGAAATTTGTTACTGTAAAAGAAGAAGTTGATGCAAACGATGTT
GAAGGTGGTAGCCTGAAAATTTTATTCAACTCTAAATATATGATGGATGCTTTAAAGCA
ATCGATAATGATGAGGTTGAAGTTGAATTTCTTCGGTACAATGAAACCATTATTCTAAAA
CCAAAAGGTGACGACTCGGTAACGCAATTAATTTTACCAATCAGAACTTACTAA

SEQ ID NO : 2 *Staphylococcus aureus* DnaN amino acid sequence

>gi|1084187|pir|S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain -
Staphylococcus aureus

MMEFTIKRDYFITQLNDTLKAISPRITLPILTGKIDAKEHEVILTGSSEISIEITIPKTVGDGDIVNI
SETGSVVLPGREFVDIIKKLPKDKVLSTNEQFQTLITSGHSEFNLSGLDPDQYPLLPQVSRDDAIQLSV
KVLKNVIAQTNEAVSTSETRPVLTGVNWLIIQENELICTATDSHRLAVRKLQLEDVSENKNVVIIPGKALAE
LNKIMSDNEEDIDIFFASNQVLFKVGNNVFISRLLEGHPDTRLPENYEIKLSIDNGEFYHAIDRASL
LAREGGNNVIKLSTGDDVVELSSTSPEIGTVKEEVDANDVEGGSCLKISFNSKYMDALKAIIDNDEVEVEF
FGTMKPFILPKGDDSVTQLILPIRTY

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